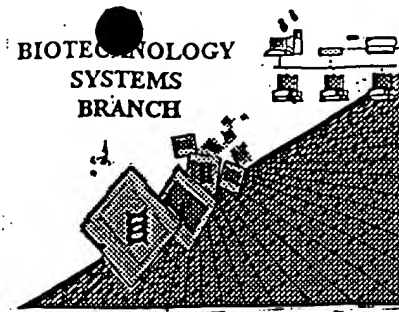


RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/988,863
Source: B1PE
Date Processed by STIC: 11/27/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/988,863

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.

- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 9 ✓ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

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OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/988,863

DATE: 11/27/2001
 TIME: 14:07:48

Input Set : A:\Pmvkl.app
 Output Set: N:\CRF3\11212001\I988863.raw

Does Not Comply
 Corrected Diskette Needed

W--> 1 SEQUENZPROTOKOLL → unnecessary for Line 1
 3 <110> APPLICANT: Bayer AG
 5 <120> TITLE OF INVENTION: Phosphomevalonat Kinasen aus Pflanzen
 7 <130> FILE REFERENCE: Le A 35 018
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/988,863
 C--> 10 <141> CURRENT FILING DATE: 2001-11-21
 12 <160> NUMBER OF SEQ ID NOS: 5
 14 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

308 <210> SEQ ID NO: 4
 309 <211> LENGTH: 728
 310 <212> TYPE: DNA
 311 <213> ORGANISM: Gossypium hirsutum
 313 <400> SEQUENCE: 4
 314 cgttttttacg ctattgttaa gccaatccat gaagctatca agcctgaaag ctgggcatgg 60
 315 tcttggaaccg atgtcaagct aacatctcct cagctttcca gagaaagcat gtataaattg 120
 316 tctcggaacac atttaacact tcagtgtgta tcttcaagtg aatcaaggaa cccttttgta 180
 317 gaaaatgcta ttcaatatac tatagcagct gcacatgcaa catttgacaa gaataagaaa 240
 318 gaggcattag ataaactact cttacaagggt cttgatatta cgatcttagg ttgcaatgac 300
 319 ttttactcat acaggaatca gatagaagca cttggtcttc cgttgacacc tgaagcattg 360
 320 gctactctac caccgtttac atcaattaca ttcaattctg aggaatcaaa tggagcaaat 420
 321 tgcaaacctg aagttgcaaa aactggattg ggttcattctg cagcaatgac aactgctgta 480
 322 gttgctgctt tacttcatta tcttggtggt gttaaccttt ccacctcttc tgcagatcaa 540
 323 caccaagaaa ataagaattc cacagatctc gatattgtgc atatgatagc tcaaagtgcc 600
 324 cactgtattg cccaaggtaa agttggcagt ggctttgatg tcagttctgc tgtctatggg 660
 E--> 325 agtcagcggt atgttcgttt ttcacaaaaa gtgctttctg ctgctcaggc tgcantgaaa 720
 326 gggatgcc 728

→ error, see error summary sheet, Item 9

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/988,863

DATE: 11/27/2001
TIME: 14:07:49

Input Set : A:\Pmvkl.app
Output Set: N:\CRF3\11212001\I988863.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:325 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4

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